

10/718480
STN Search Summary

=> d his

(FILE 'HOME' ENTERED AT 15:22:48 ON 06 OCT 2004)

FILE 'REGISTRY' ENTERED AT 15:22:57 ON 06 OCT 2004

L1 0 S LYSE/CN
L2 92 S LYSE
L3 7 S L2 AND LYSINE

FILE 'CAPLUS' ENTERED AT 15:24:09 ON 06 OCT 2004

L4 10 S L3
L5 1 S L4 AND (METHYLBACILL? OR METHYLOPHIL? OR FLAGELLAT? OR GLYCOG
L6 1 S L4 AND (METHANOL? OR METHYL?)

L3 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2004 ACS on STN
RN 615223-10-4 REGISTRY
CN Lysine exporter protein (Corynebacterium diphtheriae strain NCTC13129
gene lyse) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank CAE49614
CN GenBank CAE49614 (Translated from: GenBank BX248357)

L3 ANSWER 2 OF 7 REGISTRY COPYRIGHT 2004 ACS on STN
RN 571234-77-0 REGISTRY
CN Lysine exporter protein (Corynebacterium efficiens strain YS-314 gene
lyse) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank BAC18167
CN GenBank BAC18167 (Translated from: GenBank AP005218)

L3 ANSWER 3 OF 7 REGISTRY COPYRIGHT 2004 ACS on STN
RN 478431-27-5 REGISTRY
CN 1-125-Protein (Corynebacterium lactofermentum gene lyse) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 9: PN: EP1266966 SEQID: 10 claimed protein
CN Protein (Corynebacterium lactofermentum gene lyse24
lysine-exporting)
CN Transport protein (Corynebacterium lactofermentum gene lyse24
lysine-exporting)

L3 ANSWER 4 OF 7 REGISTRY COPYRIGHT 2004 ACS on STN
RN 338802-47-4 REGISTRY
CN Lysine-transporting protein (Corynebacterium thermoaminogenes strain
AJ12310 gene lyse) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 16: PN: JP2001120270 SEQID: 14 claimed protein

L3 ANSWER 5 OF 7 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 314317-10-7 REGISTRY
 CN Protein MP (metabolic pathway) (Corynebacterium glutamicum strain ATCC_13032 clone RXC01796) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 10: PN: WO0100843 SEQID: 10 claimed protein
 CN 16: PN: WO0166573 SEQID: 16 claimed protein
 CN Lysine-transporting protein (Corynebacterium glutamicum strain ATCC10032 clone RXC01796 gene lysE)

L3 ANSWER 6 OF 7 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 314317-08-3 REGISTRY
 CN Protein MP (metabolic pathway) (Corynebacterium glutamicum strain ATCC_13032 clone RXC02390) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 14: PN: WO0166573 SEQID: 14 claimed protein
 CN 8: PN: WO0100843 SEQID: 8 claimed protein
 CN Lysine-transporting protein (Corynebacterium glutamicum strain ATCC13032 clone RXC02390 gene lysE)

L3 ANSWER 7 OF 7 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 184922-77-8 REGISTRY
 CN Lysine-transporter (Corynebacterium glutamicum strain R127 gene lysE) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 3454: PN: EP1108790 SEQID: 6955 claimed protein
 CN Lysine exporter protein (Corynebacterium glutamicum strain R127 lysE gene)
 CN Lysine-transporting protein (Corynebacterium glutamicum strain R127 lysE gene)
 CN Protein (Corynebacterium glutamicum strain ATCC13032 clone EP1108790-SEQID-6955)
 CN Protein (Corynebacterium glutamicum strain R127 gene lysE)

L4 ANSWER 1 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2003:904048 CAPLUS
 TI The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC13129
 AU Cerdano-Tarraga, A. M.; Efstratiou, A.; Dover, L. G.; Holden, M. T. G.; Pallen, M.; Bentley, S. D.; Besra, G. S.; Churcher, C.; James, K. D.; De Zoysa, A.; Chillingworth, T.; Cronin, A.; Dowd, L.; Feltham, T.; Hamlin, N.; Holroyd, S.; Jagels, K.; Moule, S.; Quail, M. A.; Rabinowitsch, E.; Rutherford, K. M.; Thomson, N. R.; Unwin, L.; Whitehead, S.; Barrell, B. G.; Parkhill, J.
 SO Nucleic Acids Research (2003), 31(22), 6516-6523

L4 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2003:566882 CAPLUS
 TI Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens
 AU Nishio, Yousuke; Nakamura, Yoji; Kawarabayashi, Yutaka; Usuda, Yoshihiro; Kimura, Eiichiro; Sugimoto, Shinichi; Matsui, Kazuhiko; Yamagishi, Akihiko; Kikuchi, Hisashi; Ikeo, Kazuo; Gojobori, Takashi
 SO Genome Research (2003), 13(7), 1572-1579

★
invention

L4 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2002:963758 CAPLUS

TI L-lysine or L-arginine fermentation using a methanol assimilating bacterium which secretes amino acids

IN Gunji, Yoshiya; Yasueda, Hisashi

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1266966	A2	20021218	EP 2002-12539	20020605
	EP 1266966	A3	20040114		
	JP 2003061687	A2	20030304	JP 2002-151981	20020527
	US 2003124687	A1	20030703	US 2002-166142	20020611
PRAI	JP 2001-177075	A	20010612		

L4 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2001:676795 CAPLUS

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus; Kroeger, Burkhard; Schroeder, Hartwig; Zelder, Oskar; Haberhauer, Gregor; Kim, Jun-Won; Lee, Heung-Shick; Hwang, Byung-Joon

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001066573	A2	20010913	WO 2000-IB2035	20001222
	WO 2001066573	A3	20020510		
	EP 1261718	A2	20021204	EP 2000-987602	20001222
	BR 2000017148	A	20030311	BR 2000-17148	20001222
	JP 2003525623	T2	20030902	JP 2001-565737	20001222
	ZA 2002008060	A	20031110	ZA 2002-8060	20021008
PRAI	US 2000-187970P	P	20000309		
	US 2000-606740	A	20000623		
	WO 2000-IB2035	W	20001222		

L4 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2001:574896 CAPLUS

Correction of: 2001:450980

DN 135:283981

Correction of: 135:29919

TI Complete genome sequence of Corynebacterium glutamicum ATCC 13032 and its genes and encoded proteins

IN Nakagawa, Satoshi; Mizoguchi, Hiroshi; Ando, Seiko; Hayashi, Mikiro; Ochiai, Keiko; Yokoi, Haruhiko; Tateishi, Naoko; Senoh, Akihiro; Ikeda, Masato; Ozaki, Akio

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1108790	A2	20010620	EP 2000-127688	20001218
	JP 2002191370	A2	20020709	JP 2000-405096	20001215
	US 2002197605	A1	20021226	US 2000-738626	20001218
PRAI	JP 1999-377484	A	19991216		
	JP 2000-159162	A	20000407		
	JP 2000-280988	A	20000803		

L4 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2001:324284 CAPLUS
 TI Corynebacterium thermoaminogenes thermostable L-lysine biosynthesis genes
 IN Itaya, Hiroshi; Kimura, Eiichiro; Kawahara, Yoshio; Sugimoto, Shinichi
 LA Japanese

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 2001120270	A2	20010508	JP 1999-311148	19991101
PRAI	JP 1999-311148		19991101		

L4 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2001:12637 CAPLUS
 TI Corynebacterium glutamicum genes encoding proteins involved in metabolic pathways
 IN Pompejus, Markus; Kroger, Burkhard; Schroder, Hartwig; Zelder, Oskar; Haberhauer, Gregor

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001000843	A2	20010104	WO 2000-IB923	20000623
	BR 2000011806	A	20020514	BR 2000-11806	20000623
	TR 200103707	T2	20020923	TR 2001-200103707	20000623
	EP 1257649	A2	20021120	EP 2000-938999	20000623
	US 2004030116	A1	20040212	US 2003-627476	20030725
	US 2004180408	A1	20040916	US 2004-781014	20040217
PRAI	US 1999-141031P	P	19990625		
	DE 1999-19930476	A	19990701		
	US 1999-142101P	P	19990702		
	DE 1999-19931415	A	19990708		
	DE 1999-19931418	A	19990708		
	DE 1999-19931419	A	19990708		
	DE 1999-19931420	A	19990708		
	DE 1999-19931424	A	19990708		
	DE 1999-19931428	A	19990708		
	DE 1999-19931434	A	19990708		
	DE 1999-19931435	A	19990708		
	DE 1999-19931443	A	19990708		
	DE 1999-19931453	A	19990708		
	DE 1999-19931457	A	19990708		
	DE 1999-19931465	A	19990708		
	DE 1999-19931478	A	19990708		
	DE 1999-19931510	A	19990708		
	DE 1999-19931541	A	19990708		
	DE 1999-19931573	A	19990708		
	DE 1999-19931592	A	19990708		
	DE 1999-19931632	A	19990708		
	DE 1999-19931634	A	19990708		
	DE 1999-19931636	A	19990708		
	DE 1999-19932125	A	19990709		
	DE 1999-19932126	A	19990709		
	DE 1999-19932130	A	19990709		
	DE 1999-19932186	A	19990709		
	DE 1999-19932206	A	19990709		
	DE 1999-19932227	A	19990709		
	DE 1999-19932228	A	19990709		
	DE 1999-19932229	A	19990709		
	DE 1999-19932230	A	19990709		
	DE 1999-19932922	A	19990714		

DE 1999-19932926	A	19990714
DE 1999-19932928	A	19990714
DE 1999-19933004	A	19990714
DE 1999-19933005	A	19990714
DE 1999-19933006	A	19990714
US 1999-148613P	P	19990812
DE 1999-19940764	A	19990827
DE 1999-19931412	A	19990708
DE 1999-19931413	A	19990708
DE 1999-19931431	A	19990708
DE 1999-19931433	A	19990708
DE 1999-19931454	A	19990708
DE 1999-19931562	A	19990708
DE 1999-19931563	A	19990708
DE 1999-19932122	A	19990709
DE 1999-19932124	A	19990709
DE 1999-19932128	A	19990709
DE 1999-19932180	A	19990709
DE 1999-19932182	A	19990709
DE 1999-19932190	A	19990709
DE 1999-19932191	A	19990709
DE 1999-19932209	A	19990709
DE 1999-19932212	A	19990709
US 1999-143208P	P	19990709
DE 1999-19932924	A	19990714
DE 1999-19932927	A	19990714
DE 1999-19932973	A	19990714
DE 1999-19940765	A	19990827
DE 1999-19940766	A	19990827
DE 1999-19940830	A	19990827
DE 1999-19940831	A	19990827
DE 1999-19940832	A	19990827
DE 1999-19940833	A	19990827
DE 1999-19941378	A	19990831
DE 1999-19941379	A	19990831
DE 1999-19941395	A	19990831
US 1999-151572P	P	19990831
DE 1999-19942076	A	19990903
DE 1999-19942077	A	19990903
DE 1999-19942078	A	19990903
DE 1999-19942079	A	19990903
DE 1999-19942086	A	19990903
DE 1999-19942087	A	19990903
DE 1999-19942088	A	19990903
DE 1999-19942095	A	19990903
DE 1999-19942123	A	19990903
DE 1999-19942125	A	19990903
US 2000-602740	A1	20000623
US 2000-602787	A1	20000623
WO 2000-IB923	W	20000623

L4 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1997:500174 CAPLUS
 TI Microorganism amino acid exporter or gene for use in amino acid production
 by fermentation
 IN Vrljic, Marina; Eggeling, Lothar; Sahm, Hermann
 LA German

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	DE 19548222	A1	19970626	DE 1995-19548222	19951222
	CA 2241111	AA	19970703	CA 1996-2241111	19961218
	WO 9723597	A2	19970703	WO 1996-DE2485	19961218
	WO 9723597	A3	19971023		
	AU 9719218	A1	19970717	AU 1997-19218	19961218
	AU 724536	B2	20000921		
	EP 868527	A2	19981007	EP 1996-946220	19961218
	CN 1209169	A	19990224	CN 1996-180096	19961218
	BR 9612666	A	19991005	BR 1996-12666	19961218
	JP 2000507086	T2	20000613	JP 1997-523222	19961218
	RU 2225883	C2	20040320	RU 1998-113861	19961218
	ZA 9610768	A	19980731	ZA 1996-10768	19961220
PRAI	DE 1995-19548222	A	19951222		
	WO 1996-DE2485	W	19961218		

L4 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1997:475788 CAPLUS
 TI L-Lysine export from Corynebacterium glutamicum. Physiological and
 molecular-biological characterization of the carrier-mediated export of a
 primary metabolite
 AU Vrljic, Maria-Marina
 SO Berichte des Forschungszentrums Juelich (1997), Juel-3349, 1-115 pp.
 LA German

L4 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1996:757064 CAPLUS
 TI A new type of transporter with a new type of cellular function: L-lysine
 export from Corynebacterium glutamicum
 AU Vrljic, Marina; Sham, Hermann; Eggeling, Lothar
 SO Molecular Microbiology (1996), 22(5), 815-826

10/716480
STN Search Summary 2

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FILE 'CAPLUS' ENTERED AT 17:35:10 ON 06 OCT 2004

L1 2182702 (METHYLBACILL? OR METHYLOPHIL? OR FLAGELLAT? OR GLYCOGENE? OR
METHANOL? OR METHYL?)
L2 96 L1 AND LYSE
L3 6 L2 AND LYSINE
L4 1 L1 AND LYSINE(2W)EXPORT
L5 58 L1 AND LYSINE(2W)TRANSPORT
L6 5 L1 AND LYSINE(2W)RESISTANCE
L7 1 L5 AND LYSINE(2W)ANALOG?

L4 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:301460 CAPLUS
TI Lipid synthesis in Corynebacterium glutamicum: Genetical and biochemical
investigations of acyl-CoA carboxylases
AU Tilg, Yvonne
CS Institut fur Biotechnologie, Germany
SO Berichte des Forschungszentrums Juelich (2002), Juel-3946, i-ix, 1-133
CODEN: FJBEE5; ISSN: 0366-0885
LA German

L6 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:722218 CAPLUS
TI Selection and characterization of aspartokinase feedback-insensitive
mutants of Azotobacter vinelandii
AU Ekechukwu, Chioma R.; Burns, Thomas A.; Melton, Thoyd
CS Dep. Microbiology, North Carolina State Univ., Raleigh, NC, 27695, USA
SO Applied and Environmental Microbiology (1995), 61(8), 3189-91
CODEN: AEMIDF; ISSN: 0099-2240

L6 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:144831 CAPLUS
TI Endothelium-dependent relaxation of hypertensive resistance arteries is
not impaired under all conditions
AU Li, Junyi; Bukoski, Richard D.
CS Med. Branch, Univ. Texas, Galveston, TX, 77550, USA
SO Circulation Research (1993), 72(2), 290-6
CODEN: CIRUAL; ISSN: 0009-7330

L6 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1991:629291 CAPLUS
TI Isolation of variants of Chinese hamster ovary cells with abnormally low
levels of GSH: decreased ability to cleave endocytosed disulfide bonds
AU Mandel, Richard; Ryser, Hugues J. P.; Niaki, Bijan; Ghani, Farooq; Shen,
Wei Chiang
CS Sch. Med., Boston Univ., Boston, MA, 02118, USA
SO Journal of Cellular Physiology (1991), 149(1), 60-5
CODEN: JCLLAX; ISSN: 0021-9541

L6 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1991:120274 CAPLUS
 TI Fermentative manufacture of L-lysine with Brevibacterium or
 Corynebacterium species
 IN Yoshihara, Yasuhiko; Kawahara, Yoshio; Ishii, Toshimasa
 PA Ajinomoto Co., Inc., Japan
 SO Jpn. Kokai Tokkyo Koho, 4 pp.
 CODEN: JKXXAF
 DT Patent
 LA Japanese
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 02234686	A2	19900917	JP 1989-54192	19890307
	JP 2817172	B2	19981027		
	CN 1045419	A	19900919	CN 1990-101212	19900307
	CN 1030616	B	19960103		
PRAI	JP 1989-54192	A	19890307		

L6 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1988:526016 CAPLUS
 TI Selection of regenerable maize callus cultures resistant to 5-
 methyl-DL-tryptophan, S-2-aminoethyl-L-cysteine and high levels of
 L-lysine plus L-threonine
 AU Miao, Shuhua; Duncan, David R.; Widholm, Jack
 CS Dep. Agron., Univ. Illinois, Urbana, IL, 61801, USA
 SO Plant Cell, Tissue and Organ Culture (1988), 14(1), 3-14
 CODEN: PTCEDJ; ISSN: 0167-6857

L7 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1977:167623 CAPLUS
 TI Characterization of a lysine-specific active transport
 system in Rickettsia prowazeki
 AU Smith, Deborah K.; Winkler, Herbert H.
 CS Sch. Med., Univ. Virginia, Charlottesville, VA, USA
 SO Journal of Bacteriology (1977), 129(3), 1349-55
 CODEN: JOBAAY; ISSN: 0021-9193

=> d 17 abs

L7 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN
 AB R. prowazeki possesses an active transport system for lysine with a Kt of
 influx of 1 .mu.M. This intracellular lysine pool can be exchanged with
 external unlabeled substrates for a least 10 min. The lysine
 analogs L-aminoethyl cysteine, N-methyl lysine,
 hydroxylysine, and D-lysine competitively inhibited uptake of L-lysine,
 but cadaverine, diaminopimelate, arginine, ornithine, and
 .epsilon.-aminocaproate did not. Accumulation of lysine was inhibited by
 the energy poisons KCN, triphenylmethyl phosphonium Br, and
 2,4-dinitrophenol. The effect of KCN, but not 2,4-dinitrophenol or
 triphenylmethyl phosphonium Br, was overcome by ATP. Both
 energy-dependent influx and efflux were inhibited by the sulfhydryl
 reagents N-ethyl maleimide and p-chloromercuriphenyl sulfonic acid.

~~STAT~~ SEQ SEARCH SUMMARY

10/716480

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 11:16:40 ; Search time 2934 Seconds
(without alignments)
10503.373 Million cell updates/sec

Title: US-10-716-480A-1
Perfect score: 711
Sequence: 1 atggtgatcatggaaatctt.....aactgatgttgatgggtag 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
	1	711	100.0	711	6	AX643028	✓	AX643028	Sequence
	2	711	100.0	822	6	AX063771	✓	AX063771	Sequence
	3	711	100.0	822	6	AX244059	✓	AX244059	Sequence
	4	711	100.0	2374	1	CGLYSEG	✓	X96471	C.glutamicu
	5	711	100.0	2374	6	A93933	✓	A93933	Sequence 2
c	6	711	100.0	333150	1	AP005277	✓	AP005277	Corynebac
c	7	711	100.0	349980	6	AX127147	✓	AX127147	Sequence
	8	708	99.6	708	6	AX123539	✓	AX123539	Sequence
	9	708	99.6	708	6	BD165656	✓	BD165656	Novel pol
	10	696.8	98.0	712	6	AX643030	✓	AX643030	Sequence
	11	317.6	44.7	1568	6	E54483	✓	E54483	Heat-resist
	12	317.6	44.7	1771	1	AB083133	✓	AB083133	Corynebac
c	13	317.6	44.7	308650	1	AP005218	✓	AP005218	Corynebac
c	14	136.6	19.2	349535	1	BX248357	✓	BX248357	Corynebac
	15	84.2	11.8	190050	1	AL646059	✓	AL646059	Ralstonia
c	16	65.8	9.3	300861	1	AE016777	✓	AE016777	Pseudomon
	17	65.6	9.2	303550	1	SCO939131	✓	AL939131	Streptomy
	18	63.4	8.9	10542	1	AE004852	✓	AE004852	Pseudomon
c	19	63.2	8.9	10024	1	AE015725	✓	AE015725	Shewanell
c	20	62.8	8.8	24336	1	AE008841	✓	AE008841	Salmonell
c	21	62.8	8.8	298300	1	AP005025	✓	AP005025	Streptomy
	22	62.2	8.7	311600	1	AE016871	✓	AE016871	Pseudomon
c	23	62	8.7	10313	1	AE015304	✓	AE015304	Shigella
c	24	62	8.7	10701	1	AE005522	✓	AE005522	Escherich
c	25	62	8.7	266658	1	AP002563	✓	AP002563	Escherich
c	26	62	8.7	292906	1	AE016988	✓	AE016988	Shigella
	27	61.6	8.7	4033	1	ASU65741	✓	U65741	Aeromonas s
c	28	61.2	8.6	230050	1	AL627277	✓	AL627277	Salmonell
c	29	61.2	8.6	301574	1	AE016844	✓	AE016844	Salmonell
	30	60.4	8.5	636	6	E49392	✓	E49392	Process for
	31	60.4	8.5	636	6	AX030085	✓	AX030085	Sequence
	32	60.4	8.5	8029	1	ECFDAPGK	✓	X14436	Escherichia
c	33	60.4	8.5	10362	1	AE000375	✓	AE000375	Escherich

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 09:28:59 ; Search time 355 Seconds
(without alignments)
8508.363 Million cell updates/sec

Title: US-10-716-480A-1
Perfect score: 711
Sequence: 1 atggtgatcatggaaatctt.....aactgatgttgatgggtag 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	711	100.0	711	8	ACC80941	Acc80941 LysE prot
2	711	100.0	822	4	AAF71779	Aaf71779 Corynebac
3	711	100.0	822	4	AAS96098	Aas96098 C. glutam
4	711	100.0	2374	2	AAT96816	Aat96816 DNA encod
5	711	100.0	2374	9	ADB66196	Adb66196 DNA fragm
c 6	711	100.0	349980	5	AAH68528	Aah68528 C glutami
7	708	99.6	708	5	AAH68420	Aah68420 C glutami
8	696.8	98.0	712	8	ACC80942	Acc80942 LysE24 pr
9	317.6	44.7	1568	4	AAH45375	Aah45375 C. thermo
10	60.4	8.5	636	3	AAA52691	Aaa52691 Escherich

OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 12:21:55 ; Search time 83 Seconds
(without alignments)
4753.856 Million cell updates/sec

Title: US-10-716-480A-1
Perfect score: 711
Sequence: 1 atggtgatcatggaaatctt.....aactgatgttgatgggtag 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	Query	Match	Length	DB	ID		
No.	Score						
c	1	61.8	8.7	699	4	US-09-252-991A-7908	Sequence 7908, Ap
	2	61.8	8.7	834	4	US-09-252-991A-7643	Sequence 7643, Ap
	3	61.8	8.7	894	4	US-09-252-991A-7841	Sequence 7841, Ap
c	4	57	8.0	597	4	US-09-894-844-11	Sequence 11, Appl
	5	57	8.0	15239	1	US-08-390-878-17	Sequence 17, Appl
	6	57	8.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	7	57	8.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	8	56.6	8.0	642	4	US-09-489-039A-4674	Sequence 4674, Ap
	9	53.8	7.6	1176	4	US-09-252-991A-7571	Sequence 7571, Ap
c	10	43	6.0	645	4	US-09-543-681A-800	Sequence 800, App
	11	39.4	5.5	505	4	US-09-621-976-15639	Sequence 15639, A
	12	37.6	5.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	711	100.0	711	15	US-10-166-142-7	Sequence 7, Appli	
2	711	100.0	711	17	US-10-716-473-7	Sequence 7, Appli	
3	711	100.0	822	10	US-09-746-660A-51	Sequence 51, Appl	
4	711	100.0	2374	15	US-10-196-232-24	Sequence 24, Appl	
c 5	711	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli	
6	708	99.6	708	9	US-09-738-626-3455	Sequence 3455, Ap	
7	696.8	98.0	712	15	US-10-166-142-9	Sequence 9, Appli	
8	696.8	98.0	712	17	US-10-716-473-9	Sequence 9, Appli	
9	62.8	8.8	609	15	US-10-156-761-1109	Sequence 1109, Ap	
c 10	62.8	8.8	9025608	15	US-10-156-761-1	Sequence 1, Appli	
11	57	8.0	597	9	US-09-894-844-11	Sequence 11, Appl	
12	57	8.0	597	13	US-10-647-089-11	Sequence 11, Appl	
13	57	8.0	597	16	US-10-388-902-11	Sequence 11, Appl	
14	56.2	7.9	86114	15	US-10-080-170-648	Sequence 648, App	
15	56.2	7.9	86114	17	US-10-080-170-648	Sequence 648, App	
c 16	42.2	5.9	1780	17	US-10-437-963-18491	Sequence 18491, A	
17	42.2	5.9	3000	15	US-10-156-761-5949	Sequence 5949, Ap	
18	42.2	5.9	9025608	15	US-10-156-761-1	Sequence 1, Appli	
19	42	5.9	2301	17	US-10-437-963-6293	Sequence 6293, Ap	
20	41.2	5.8	2016	17	US-10-437-963-86805	Sequence 86805, A	
21	40.4	5.7	1392	16	US-10-369-493-31368	Sequence 31368, A	
22	40.4	5.7	1443	16	US-10-369-493-28610	Sequence 28610, A	
23	40.4	5.7	2429	17	US-10-437-963-6292	Sequence 6292, Ap	
c 24	40	5.6	3483	17	US-10-437-963-44614	Sequence 44614, A	
c 25	39.4	5.5	594	16	US-10-369-493-33277	Sequence 33277, A	
c 26	39.2	5.5	752	17	US-10-437-963-23986	Sequence 23986, A	
c 27	39.2	5.5	1257	15	US-10-156-761-5999	Sequence 5999, Ap	
c 28	39	5.5	993	10	US-09-746-660A-47	Sequence 47, Appl	
29	39	5.5	2823	13	US-10-282-122A-26243	Sequence 26243, A	
30	39	5.5	2826	13	US-10-282-122A-28428	Sequence 28428, A	
31	38.6	5.4	1245	13	US-10-282-122A-14346	Sequence 14346, A	
32	38.4	5.4	1236	17	US-10-437-963-95996	Sequence 95996, A	
c 33	38.2	5.4	1365	17	US-10-437-963-14494	Sequence 14494, A	
c 34	38	5.3	1018	13	US-10-425-114-960	Sequence 960, App	
35	38	5.3	1458	15	US-10-156-761-1306	Sequence 1306, Ap	
c 36	38	5.3	2218	13	US-10-425-114-28221	Sequence 28221, A	
c 37	38	5.3	2457	13	US-10-425-114-30614	Sequence 30614, A	
38	37.8	5.3	270	17	US-10-437-963-34340	Sequence 34340, A	
c 39	37.8	5.3	536	17	US-10-338-110-119	Sequence 119, App	
40	37.8	5.3	2038	15	US-10-094-113-11	Sequence 11, Appl	
41	37.6	5.3	536	17	US-10-338-110-119	Sequence 119, App	
c 42	37.6	5.3	2079	15	US-10-156-761-1755	Sequence 1755, Ap	
c 43	37.6	5.3	3073	13	US-10-424-599-33204	Sequence 33204, A	
c 44	37.6	5.3	3090	13	US-10-425-114-11304	Sequence 11304, A	
45	37.4	5.3	624	15	US-10-156-761-2439	Sequence 2439, Ap	

ALIGNMENTS

RESULT 1
US-10-166-142-7

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OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 12:24:20 ; Search time 2516 Seconds
(without alignments)
8438.796 Million cell updates/sec

Title: US-10-716-480A-1
Perfect score: 711
Sequence: 1 atggtgatcatggaaatctt.....aactgatgttgatgggtag 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      October 7, 2004, 15:19:08 ; Search time 2849 Seconds  
            (without alignments)  
            3590.367 Million cell updates/sec
```

Title: US-10-716-480A-2
Perfect score: 1191
Sequence: 1 MVIMEIFITGLLLGASLLLS.....INVVVAVVMTALAIKLMLMG 236

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext 7.0
```

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=xlp
```

Q=/cgn2_1/USPTO_spool_p/US10716480/runat_06102004_102309_20226/app_query.fasta_1
.391

```
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10716480_@CGN_1_1_5600_@runat_06102004_102309_20226 -NCPU=6 -ICPU=3
-NO_MMMap -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
```

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*
 15: em_ba:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_mu:*
 20: em_om:*
 21: em_or:*
 22: em_ov:*
 23: em_pat:*
 24: em_ph:*
 25: em_pl:*
 26: em_ro:*
 27: em_sts:*
 28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query							
Result	No.	Score	Match	Length	DB	ID	Description				
	1	1191	100.0	708	6	AX123539	Nakagami	6/100	25	AX123539	Sequence
	2	1191	100.0	708	6	BD165656	"	6/100	JP	BD165656	Novel pol
	3	1191	100.0	711	6	AX643028	Applicon	6/100	WO	AX643028	Sequence
	4	1191	100.0	822	6	AX063771	Pomifus	6/100	WO	AX063771	Sequence
	5	1191	100.0	822	6	AX244059	"	6/100	WO	AX244059	Sequence
	6	1191	100.0	2374	1	CGLYSEG	Vrijic	6/100	WO	X96471	C.glutamicu
	7	1191	100.0	2374	6	A93933	"	6/100	WO	A93933	Sequence 2
c	8	1191	100.0	333150	1	AP005277	Nakagami	6/100	JP	AP005277	Corynebac
c	9	1191	100.0	349980	6	AX127147	Applicon	6/100	EP	AX127147	Sequence
	10	1169	98.2	712	6	AX643030	Applicon	6/100	EP	AX643030	Sequence
	11	864.5	72.6	1568	6	E54483	Itanaka	6/100	JP	E54483	Heat-resist
	12	864.5	72.6	1771	1	AB083133	Itanaka	6/100	JP	AB083133	Corynebac
c	13	864.5	72.6	308650	1	AP005218	"	6/100	JP	AP005218	Corynebac
c	14	562	47.2	349535	1	BX248357	Nakagami	6/100	JP	BX248357	Corynebac
	15	352	29.6	636	6	E49392	"	6/100	JP	E49392	Process for
	16	352	29.6	636	6	AX030085	"	6/100	JP	AX030085	Sequence

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OM protein - nucleic search, using frame_plus_p2n model

```
Run on:      October 7, 2004, 14:30:02 ; Search time 340 Seconds
              (without alignments)
              2948.749 Million cell updates/sec
```

```
Title:          US-10-716-480A-2
Perfect score: 1191
Sequence:      1 MVIMEIFITGLLLGASLLLS.....INVVVAVVMTALAIKLMLMG 236
```

```

Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop   6.0 , Delext  7.0

```

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=xlp
```

Q=/cgn2_1/USPTO_spool_p/US10716480/runat_06102004_102309_20217/app_query.fasta_1
.391

```
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10716480 @CGN_1_1_708 @runat_06102004_102309_20217 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      N_Geneseq_29Jan04:*
              1:  geneseqn1980s:*
              2:  geneseqn1990s:*
              3:  geneseqn2000s:*
              4:  geneseqn2001as:*
              5:  geneseqn2001bs:*
              6:  geneseqn2002s:*
              7:  geneseqn2003as:*
              8:  geneseqn2003bs:*
              9:  geneseqn2003cs:*
             10:  geneseqn2004s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1191	100.0	708	5	AAH68420	Aah68420 C glutami
2	1191	100.0	711	8	ACC80941	Acc80941 LysE prot
3	1191	100.0	822	4	AAF71779	Aaf71779 Corynebac
4	1191	100.0	822	4	AAS96098	Aas96098 C. glutam
5	1191	100.0	2374	2	AAT96816	Aat96816 DNA encod
6	1191	100.0	2374	9	ADB66196	Adb66196 DNA fragm
c 7	1191	100.0	349980	5	AAH68528	Aah68528 C glutami
8	1169	98.2	712	8	ACC80942	Acc80942 LysE24 pr
9	864.5	72.6	1568	4	AAH45375	Aah45375 C. thermo
* 10	352	29.6	636	3	AAA52691	Aaa52691 Escherich
11	327.5	27.5	86114	6	ABX09143	Abx09143 Mycobacte
12	327.5	27.5	110000	4	AAI99682_05	Continuation (6 of
13	327.5	27.5	110000	4	AAI99683_05	Continuation (6 of
c 14	318	26.7	15239	2	AAT33536	Aat33536 BCG delet
15	318	26.7	110000	4	AAI99682_22	Continuation (23 o
16	318	26.7	110000	4	AAI99683_22	Continuation (23 o
17	298	25.0	624	7	ACF71727	Acf71727 Photorhab
18	298	25.0	636	8	ADA30324	Ada30324 DNA encod
19	298	25.0	110000	7	ACF67367_49	Continuation (50 o
20	298	25.0	110000	7	ACF65387_0	Acf65387 Photorhab
21	170.5	14.3	630	2	AAT67601	Aat67601 H. pylori
22	170.5	14.3	645	2	AAT68221	Aat68221 H. pylori
23	165	13.9	7521	5	AAS71378	Aas71378 DNA encod
24	165	13.9	7521	5	AAS94251	Aas94251 DNA encod
25	164	13.8	615	7	ACF73766	Acf73766 Staphyloc
26	154.5	13.0	3520	4	AAH54185	Aah54185 S. epider
27	135.5	11.4	110000	7	ACF67367_28	Continuation (29 o
c 28	135.5	11.4	110000	7	ACF65386_0	Acf65386 Photorhab
29	132.5	11.1	615	7	ACF69801	Acf69801 Photorhab
30	132.5	11.1	678	5	AAH65130	Aah65130 C glutami
31	132.5	11.1	678	7	ACA01893	Aca01893 C. glutam
32	132.5	11.1	349980	5	AAH64966	Aah64966 C glutami
33	121.5	10.2	708	8	ADA32836	Ada32836 DNA encod
34	121	10.2	405	2	AAV75577	Aav75577 Staphyloc
35	119.5	10.0	522	6	ABN91726	Abn91726 Staphyloc
36	119.5	10.0	669	8	ADA31058	Ada31058 DNA encod
37	119	10.0	1863	7	ACA53564	Aca53564 Prokaryot
c 38	116	9.7	110000	7	ACF65385_1	Continuation (2 of
c 39	116	9.7	110000	7	ACF67367_30	Continuation (31 o
c 40	114.5	9.6	1668	3	AAA61501	Aaa61501 A. vitis
41	114.5	9.6	1668	3	AAA61502	Aaa61502 A. vitis
42	112	9.4	609	7	ACF70009	Acf70009 Photorhab
43	108.5	9.1	636	7	ACF68771	Acf68771 Photorhab
44	108.5	9.1	717	8	ADA31709	Ada31709 DNA encod
45	108.5	9.1	110000	7	ACF67367_15	Continuation (16 o

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      October 7, 2004, 16:03:58 ; Search time 81 Seconds
              (without alignments)
              1616.894 Million cell updates/sec
```

Title: US-10-716-480A-2
Perfect score: 1191
Sequence: 1 MVIMEIFITGLLLGASLLLS.....INVVVAVVMTALAIKLMLMG 236

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop 6.0 , Delext 7.0
```

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=xlp
```

Q=/cgn2_1/USPTO_spool_p/US10716480/runat_06102004_102310_20256/app_query.fasta_1
.391

```
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10716480_CGN_1_1_105@runat_06102004_102310_20256 -NCPU=6 -ICPU=3
-NO_MMMap -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      Issued_Patents_NA:*
1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3:  /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4:  /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	341	28.6	642	4	US-09-489-039A-4674	Sequence 4674, Ap
	2	332	27.9	699	4	US-09-252-991A-7908	Sequence 7908, Ap
c	3	332	27.9	834	4	US-09-252-991A-7643	Sequence 7643, Ap
	4	332	27.9	894	4	US-09-252-991A-7841	Sequence 7841, Ap
	5	327.5	27.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	6	327.5	27.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	7	318	26.7	597	4	US-09-894-844-11	Sequence 11, Appl
c	8	318	26.7	15239	1	US-08-390-878-17	Sequence 17, Appl
	9	310	26.0	645	4	US-09-543-681A-800	Sequence 800, App
	10	298	25.0	636	4	US-09-328-352-1611	Sequence 1611, Ap
c	11	157	13.2	1176	4	US-09-252-991A-7571	Sequence 7571, Ap
	12	138.5	11.6	639	4	US-09-543-681A-595	Sequence 595, App
	13	135.5	11.4	783	4	US-09-252-991A-9421	Sequence 9421, Ap
	14	135.5	11.4	1596	4	US-09-252-991A-9478	Sequence 9478, Ap
c	15	135.5	11.4	1650	4	US-09-252-991A-9352	Sequence 9352, Ap
	16	121.5	10.2	708	4	US-09-328-352-4123	Sequence 4123, Ap
	17	121	10.2	405	4	US-08-956-171E-1266	Sequence 1266, Ap
	18	119.5	10.0	522	4	US-09-134-001C-1189	Sequence 1189, Ap
	19	119.5	10.0	669	4	US-09-328-352-2345	Sequence 2345, Ap
	20	118.5	9.9	753	4	US-09-543-681A-315	Sequence 315, App
c	21	118.5	9.9	1713	4	US-09-252-991A-9760	Sequence 9760, Ap
	22	118.5	9.9	2805	4	US-09-252-991A-10208	Sequence 10208, A
	23	117.5	9.9	621	4	US-09-252-991A-2175	Sequence 2175, Ap
c	24	117.5	9.9	813	4	US-09-252-991A-1792	Sequence 1792, Ap
	25	115.5	9.7	660	4	US-09-489-039A-560	Sequence 560, App
	26	113.5	9.5	687	4	US-09-543-681A-682	Sequence 682, App
	27	111	9.3	669	4	US-09-252-991A-10073	Sequence 10073, A
	28	108.5	9.1	717	4	US-09-328-352-2996	Sequence 2996, Ap
	29	108	9.1	654	4	US-09-489-039A-905	Sequence 905, App
	30	104.5	8.8	636	4	US-09-543-681A-2536	Sequence 2536, Ap
	31	104	8.7	750	4	US-09-252-991A-9146	Sequence 9146, Ap
c	32	103	8.6	1650	4	US-09-489-039A-1643	Sequence 1643, Ap
	33	103	8.6	3324	4	US-09-489-039A-1719	Sequence 1719, Ap
	34	101.5	8.5	663	4	US-09-328-352-777	Sequence 777, App
	35	99	8.3	627	4	US-09-328-352-985	Sequence 985, App
	36	97.5	8.2	636	4	US-09-489-039A-2437	Sequence 2437, Ap
c	37	96	8.1	3402	4	US-09-252-991A-1374	Sequence 1374, Ap
	38	96	8.1	3687	4	US-09-252-991A-1193	Sequence 1193, Ap
	39	96	8.1	4266	4	US-09-252-991A-1234	Sequence 1234, Ap
	40	94.5	7.9	723	4	US-09-328-352-3411	Sequence 3411, Ap
	41	94	7.9	1659	4	US-09-489-039A-248	Sequence 248, App
	42	93	7.8	687	4	US-09-252-991A-7266	Sequence 7266, Ap
c	43	93	7.8	1521	4	US-09-252-991A-7437	Sequence 7437, Ap
	44	93	7.8	2397	4	US-09-252-991A-7203	Sequence 7203, Ap
c	45	91.5	7.7	7754	4	US-09-634-238-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-489-039A-4674

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      October  7, 2004, 16:11:23 ; Search time 407 Seconds
              (without alignments)
              2939.601 Million cell updates/sec
```

Title: US-10-716-480A-2
Perfect score: 1191
Sequence: 1 MVIMEIFITGLLLGASLLLS.....INVVVAVVMTALAIKLMIMG 236

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0
```

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=xlp
```

Q=/cgn2_1/USPTO_spool_p/US10716480/runat_06102004_102310_20286/app_query.fasta_1
.391

```
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10716480_CGN_1_1_783@runat_06102004_102310_20286
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
```

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Query Match Length DB ID			
	1	1191	100.0	708	9	US-09-738-626-3455 <i>NAK US</i> Sequence 3455, Ap
	2	1191	100.0	711	15	US-10-166-142-7 <i>NAK</i> Sequence 7, Appli
	3	1191	100.0	711	17	US-10-716-473-7 <i>NAK</i> Sequence 7, Appli
	4	1191	100.0	822	10	US-09-746-660A-51 <i>POMP US</i> Sequence 51, Appl
	5	1191	100.0	2374	15	US-10-196-232-24 <i>YOMA</i> Sequence 24, Appl
c	6	1191	100.0	3309400	9	US-09-738-626-1 <i>NAK</i> Sequence 1, Appli
	7	1169	98.2	712	15	US-10-166-142-9 <i>NAK</i> Sequence 9, Appli
	8	1169	98.2	712	17	US-10-716-473-9 <i>NAK</i> Sequence 9, Appli
	9	327.5	27.5	86114	15	US-10-080-170-648 Sequence 648, App
	10	327.5	27.5	86114	17	US-10-080-170-648 Sequence 648, App
	11	318	26.7	597	9	US-09-894-844-11 Sequence 11, Appl
	12	318	26.7	597	13	US-10-647-089-11 Sequence 11, Appl
	13	318	26.7	597	16	US-10-388-902-11 Sequence 11, Appl
	14	301	25.3	609	15	US-10-156-761-1109 Sequence 1109, Ap
c	15	301	25.3	9025608	15	US-10-156-761-1 Sequence 1, Appli
	16	170.5	14.3	630	13	US-10-335-977-1122 Sequence 1122, Ap
	17	170.5	14.3	633	13	US-10-335-977-1121 Sequence 1121, Ap
	18	170.5	14.3	645	13	US-10-335-977-1123 Sequence 1123, Ap
	19	133	11.2	672	15	US-10-156-761-246 Sequence 246, App
	20	132.5	11.1	678	9	US-09-738-626-165 Sequence 165, App
	21	132.5	11.1	3309400	9	US-09-738-626-1 Sequence 1, Appli
	22	128.5	10.8	32329	13	US-10-374-903A-1 Sequence 1, Appli
	23	121	10.2	405	8	US-08-781-986A-1266 Sequence 1266, Ap
	24	121	10.2	405	13	US-10-329-624-1266 Sequence 1266, Ap
	25	119	10.0	1863	13	US-10-282-122A-41434 Sequence 41434, A
	26	109.5	9.2	630	15	US-10-156-761-7444 Sequence 7444, Ap
	27	103.5	8.7	543	13	US-10-282-122A-8689 Sequence 8689, Ap
	28	99.5	8.4	888	13	US-10-282-122A-41598 Sequence 41598, A
	29	98.5	8.3	651	15	US-10-156-761-3368 Sequence 3368, Ap
	30	97.5	8.2	750	13	US-10-620-487-1 Sequence 1, Appli
	31	96.5	8.1	1018	13	US-10-425-114-28659 Sequence 28659, A
	32	94	7.9	1630	17	US-10-437-963-62711 Sequence 62711, A
	33	93.5	7.9	1359	9	US-09-815-242-6086 Sequence 6086, Ap
	34	93.5	7.9	1359	13	US-10-282-122A-20388 Sequence 20388, A
	35	93	7.8	633	13	US-10-282-122A-11642 Sequence 11642, A
	36	93	7.8	894	15	US-10-156-761-1180 Sequence 1180, Ap
	37	93	7.8	1377	9	US-09-738-626-3498 Sequence 3498, Ap
	38	93	7.8	9025608	15	US-10-156-761-1 Sequence 1, Appli

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      October 7, 2004, 16:02:13 ; Search time 2437 Seconds  
              (without alignments)  
              2891.865 Million cell updates/sec
```

Title: US-10-716-480A-2
Perfect score: 1191
Sequence: 1 MVIMEIFITGLLLGASLLLS.....INVVVAVVMTALAIKLMIMG 236

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop  6.0 , Delext   7.0
```

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=xlp
```

Q=/cgn2_1/USPTO_spool_p/US10716480/runat_06102004_102310_20237/app_query.fasta_1
.391

```
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10716480_CGN_1_1_5180@runat_06102004_102310_20237 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database : EST:*
1:  em_estba:*
2:  em_esthum:*
3:  em_estin:*
4:  em_estmu:*
5:  em_estov:*
6:  em_estpl:*
7:  em_estro:*
8:  em_htc:*
9:  gb_est1:*
10: gb_est2:*
```

11: gb_htc:*
 12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	317.5	26.7	830	29	CNS01MQH			AL151258 Anopheles
c	2	281	23.6	667	28	AQ991044			AQ991044 Rfc01899
	3	207.5	17.4	1034	28	BZ554294			BZ554294 pacs1-60_
c	4	205.5	17.3	833	28	BZ556963			BZ556963 pacs1-60_
c	5	199	16.7	804	29	CNS01HIJ			AL144476 Anopheles
c	6	160	13.4	897	28	BZ560550			BZ560550 pacs2-164
c	7	149	12.5	1620	28	BZ568946			BZ568946 pacs2-164
c	8	143	12.0	751	28	BH391509			BH391509 AG-ND-159
	9	116.5	9.8	909	28	BZ565158			BZ565158 pacs2-164
	10	98	8.2	829	28	CC113281			CC113281 NDL.24H1.
	11	94.5	7.9	1525	29	AY415555			AY415555 Pan trogl
c	12	94	7.9	840	29	CC719070			CC719070 OGWCI79TV
	13	93.5	7.9	210	14	CB020010			CB020010 pw98f01.y
	14	93.5	7.9	570	14	CF275208			CF275208 NcEST3d13
	15	93.5	7.9	741	13	BX612630			BX612630 BX612630
	16	91	7.6	632	12	BI862608			BI862608 603389677
c	17	90	7.6	798	29	CNS01QYA			AL156722 Anopheles
	18	89.5	7.5	679	13	BW283758			BW283758 BW283758
	19	89	7.5	590	14	CD482346			CD482346 atr01-4ms
	20	89	7.5	709	14	CA300534			CA300534 SCSFLV104
	21	88.5	7.4	438	28	AQ856877			AQ856877 nbeb0004K
c	22	88.5	7.4	945	13	BU554436			BU554436 AGENCOURT
c	23	88.5	7.4	1233	28	BZ579504			BZ579504 msh2_6385
c	24	87.5	7.3	628	14	CA279614			CA279614 SCCCFL800
	25	87.5	7.3	656	13	BU002594			BU002594 QGG31M20.
c	26	87.5	7.3	682	29	CC968186			CC968186 BOICV59TR
	27	87.5	7.3	684	13	BQ856142			BQ856142 QGB28L08.
	28	87.5	7.3	710	13	BQ866753			BQ866753 QGC8N13.y